



TGGATCAGATAAAAGTTTGTAAGA

ATGACAAAGAAATGAGAAGAGTGGGCAAGTACGAGGTGGTCGCACAATAGGTGAAGGAACCTTTGCTAAGGTTAAG

1 M T K K M R R V G K Y E V G R T I G E G T F A K V K

-- I --

TTTGGAGGACACAGACACTGGTGATAATGTAGCCATCAAAATTATGGCTAAGAGTACAATACTTAAGAACAGAATG

27 F A R N T D T G D N V A I K I M A K S T I L K N R M

-- II --

GTTGATCAGATAAAAGAGAGATATCTATAATGAAGATTGTTGTCACCCGAACATAGTGAGTTGTATGAGGTGTG

53 V D Q I K R E I S I M K I V R H P N I V R L Y E V L

-- III --

-- IV --

GCGAGTCCTTCGAAATATATAGTTTTGGAGTTGTGACAGGAGAGAGCTCTTTGATAGATTGTTTCATAAAGGG

79 A S P S K I Y I V L E F V T G G E L F D R I V H K G

-- V --

AGGCTTGAAGAAAGTGAGTCTCGGAAATACTTCAACAGCTTGTAGATGCTGTTGCTCATTGTCACCTGCAAGGGTGTT

105 R L E E S E S R K Y F Q Q L V D A V A H C H C K G V

-- VI --

TACCACCGTGACCTAAAGCCAGAAAATCTTTTACTCGATACAAATGGAATCTGAAGTTTCGGATTTCGGACTCAGT

131 Y H R D L K P E N L L L D T N G N L K V S D F G L S

-- VII --

GCATTGCCTCAGGAAGGAGTAGAACTTCTGCGTACCACATGTGGAACCTCCGAACATGTAGCTCCAGAGGTACTTAGT

157 A L P Q E G V E L L R T T C G T P N Y V A P E V L S

-- VIII --

FIG. 2B(1)



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GGACAGGTTACGATGGTTCAGCAGCIGATATTGGTCTTGCGGGTTATTCTTTTCGTTATATGGCTGGATATTTA
183 G Q G Y D G S A A [D] I [W] [S] C [G] [V] I L F V I L A G Y L

--IX--

CCTTTTCCGAGACGGATCTTCCAGGTTGTACAGAAAATAAATGCAGCAGAGTTTCTTGTCACCGTGGTTTCC
209 P F S E T D L P G L Y R K I N A A E F S C P P W F S

--X--

GCAGAAGTGAAGTTTTTAATACATAGGATACTTGACCCCAATCCCAAAACACGTATTCAAATTCAGGAATCAAGAAA
235 A E V K F L I H R [I] L D P N P K T R I Q [I] Q G I K K

--XI--

GATCCTTGTTTCAGATTAAATTATGTGCCTATACGAGCAAGGGAAGAAGTGAATTTGGATGATATTCGTGCA
261 D P W F R L N Y V P I R A R E E E V N L D D I R A

GTTTTGATGGAATTGAGGCGAGTTATGTAGCGGAGAAATGTAGAGAGAAATGATGAAGGCCCTGATGATGATGCC
287 V F D G I E G S Y V A E N V E R N D E G P L M N A

TTTGAGATGATTACCTTATCACAGGCTTAAATTATCTGCACTATTTGACAGCGCAGGATTTTGTAAAGGCAA
313 F E M I T L S Q G L N L S A L F D R R Q D F V K R Q

ACCGTTTTGTTTCTCGAAGGGAACCTAGTGAGATAATTGCTAACATTGAGGCTGTAGCGAAGTGGTTTAAAG
339 T R F V S R R E P S E I I A N I E A V A N S M G F K

FIG. 2B(2)



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REPLACEMENT DRAWINGS

TCTCATACAGAACTTCAAGACAAGGCTCGAGGGATTATCTTCGATCAAGGCCGGACAGTTAGCTGTTGTGATAGAG
365 S H T R N F K T R L E G L S S I K A G Q L A V V I E
ATTTACGAGGTGGCACCATCGCTTTTCATGTTAGACGTAAAGAAAGGCTGCTGGTGAACCTCTTGAATATCACAAGTTC
391 I Y E V A P S L F M V D V R K A A G E T L E Y H K F
TACAAGAAGCTATGTTCGAAACTGGAAACATAATATGGAGGGCAACAGAGGAATACCAAAGTCAGAGATTCTCAGA
417 Y K K L C S K L E N I I W R A T E G I P K S E I L R
ACAATCACGTTTGTGATCCCAACTTAA
437 T I T F

FIG. 2B(3)



*
SOS2 1 MTKMRRVGVKYEVRIGEGTFAKVKFARNDDTGDNVAIKIMAKSTLKNRMVDDQ
AMPK 1 MAEKQKHGGRVKIGHYMLGDTLGMGTFGKVKIGEHLTGKQVAVKILNRQKQKRSLDVVVGK
SNF1 45 SLADGAHTGNQJIVKTLGEGSGKVKLAYHTITGQKVALKIINKKVAKSDMQGR

IKREISIMKIVRHPNIVRLYEVLASPSKIYIVLEFVTGGELFDRIVHKGRL ESESRKYF
AMPK 61 IKREIQNLKIFRPHPHI IKLYQVISTPTDFMVMEYVSGGELFDYJCKHGRVEEMEARLE
SNF1 101 IEREISMLRLRHPHI IKLYDVJKSKDEJIMVIEYA-GNELFDYIVQRDKMSEQEARRFF

QQLVDAVAHCHCKGVHRDLKPENLLDTNGNLKVSDFGLSAQPQEGVELRTTCGTPNY
AMPK 121 QQILSAVDYCHRMVVHRDLKPENLLDAHINAKIADFGLSNMMSDG-EFLRTSCGSPNY
SNF1 161 QQIISAVEYCHRHIVHRDLKPENLLDEHLNVKIADEGLSNIMTDG-NFLKTSCGSPNY

*
SOS2 176 VAPEVLSGGQYDGSAAADIWSCGVILFVILAGYLPFSETDLPGLYRKINAAEFSCPPWFS
AMPK 180 TAPEVISGRLYAGPEVDIWSCGVILYALLCGTLPFDDEHVPITLFKKIRGGVYITPEYLN
SNF1 221 AAPEVISGKLYAGPEVDVWSCGVILYVMLQRRLPFDDDESIPVLFKNISNGVYTLPKFLSP

EVKFLIHRILDPNPKTRIQJQGIKKDPWFLN
AMPK 240 SVATILMHMLQVDPKRAITIKDIRHEWFKQG
SNF1 282 GAAGLIKRMILVNPNRISIEHJMQDDWFKVD

FIG. 3A



SOS2 332 QDFVKRQTRFMSRREPSEIJANIEAVANSMGFKS---HTRNFKTRLEGSSIKAGQAVM
CHK1 389 ICPPELRFYSRASRETIIDHIDYDSLRLAISVTMKYVRNQTIDVNNHDKRKCLQGV
CHK1 371 QRLVKRMTRFFTKLDADKSYQCCKETCEKLGW---KSCMNQVTISITDRRNNKIFK

SOS2 389 IETIYEVAPSQFMVDVRKAAGETLEYHKFYKKCSKLENITWRATEGIP
CHK1 449 IELTNLGHNEELINFJIKRNGDPLEWRKFFKNVSSIGKPIVLTDMSON
CHK1 428 VNLLEMD-DKILVDFRLSKGDGLEFKRHLKIKGKLIIDIVSSQKMLP

FIG. 3B



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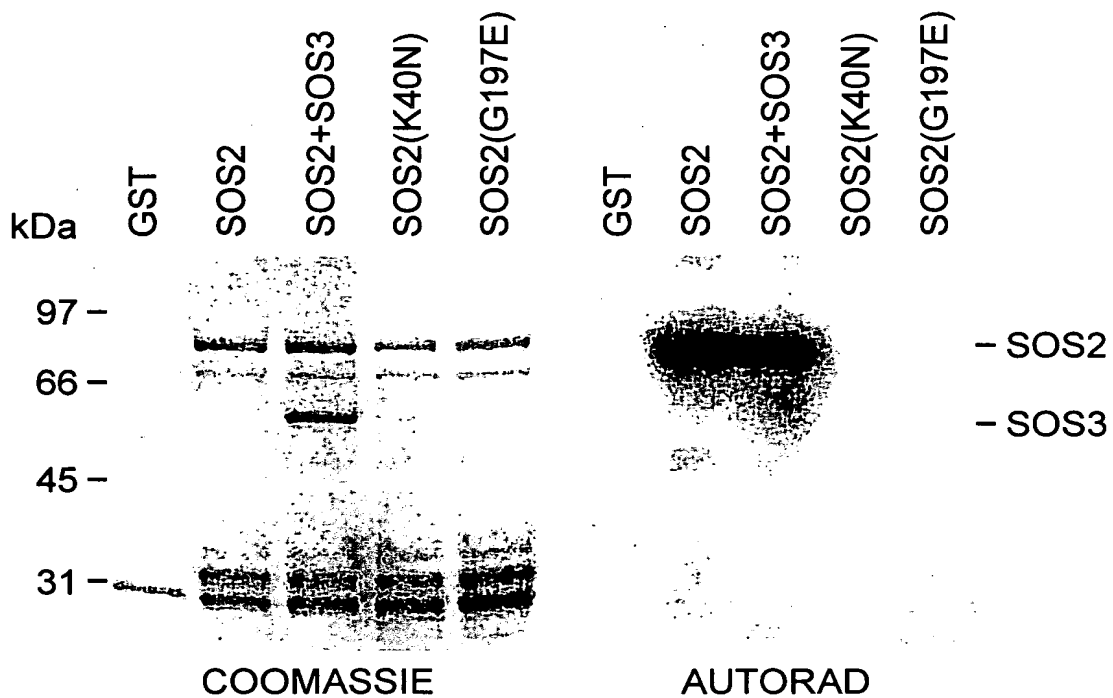


FIG.4

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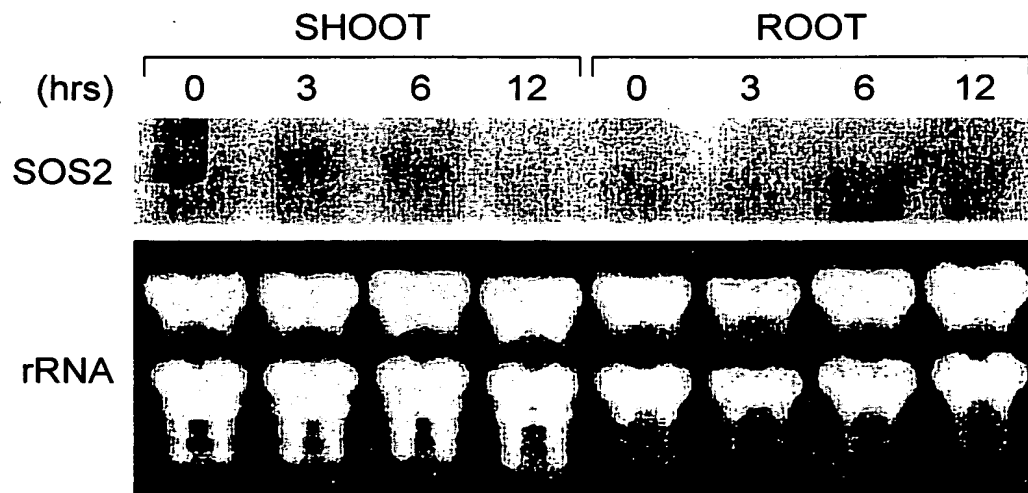


FIG.5A

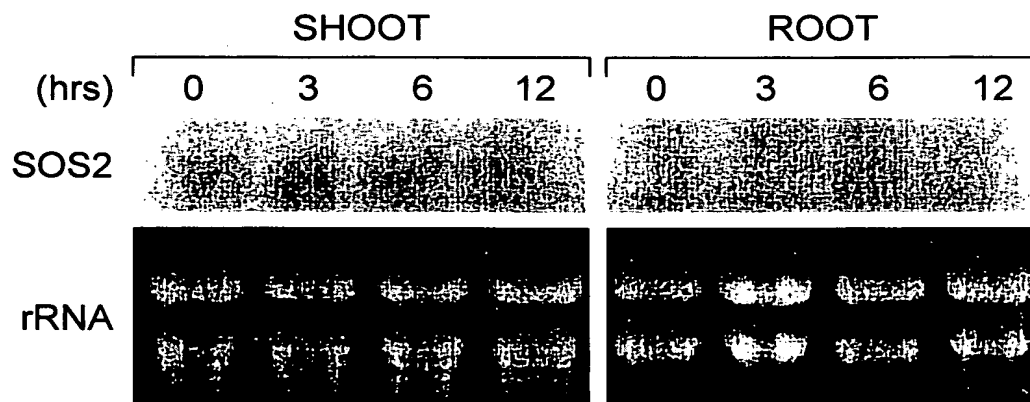


FIG.5B